

SEQUENCE LISTING

<110> Prof. Dr. Werner Seeger
 <120> Novel chimeric plasminogen activators and their pharmaceutical use
 <160> 13
 <210> 1
 <211> 1143
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1) ... (1143)
 <223> Coding sequence of the surfactant protein B precursor
 <400> 1

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg gac aag ctc	528

Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu			
165	170	175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac		576	
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His			
180	185	190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc		624	
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys			
195	200	205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag		672	
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys			
210	215	220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg		720	
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu			
225	230	235	240
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc		768	
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile			
245	250	255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc		816	
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg			
260	265	270	
ctc gtc ctc cgg tgc tcc atg gat gac agc gct ggc cca agg tcc ccg		864	
Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro			
275	280	285	
aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc		912	
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser			
290	295	300	
gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca		960	
Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala			
305	310	315	320
atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag		1008	
Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys			
325	330	335	
caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg		1056	
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg			
340	345	350	
ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc		1104	
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr			
355	360	365	
atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt		1143	
Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu			
370	375	380	

<210> 2

<211> 837

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<400> 2

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
) aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
) aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624

Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys			
195	200	205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag			672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys			
210	215	220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg			720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu			
225	230	235	240
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc			768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile			
245	250	255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc			816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg			
260	265	270	
ctc gtc ctc cgg tgc tcc atg			837
Leu Val Leu Arg Cys Ser Met			
275			
<210> 3			
<211> 237			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (1) ... (237)			
<223> Coding sequence of the mature surfactant protein B			
<400> 3			
ttc ccc att cct ctc ccc tat tgc tgg ctc tgc agg gct ctg atc aag			48
Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys			
1	5	10	15
cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc			96
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala			
20	25	30	
cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc atc tgc cag tgc			144
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys			
35	40	45	
ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc			192
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg			
50	55	60	
atg ctg ccc cag ctg gtc tgc cgc ctc gtc cgg tgc tcc atg			237
Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met			
65	70	75	

<210> 4
<211> 1293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1293)

<223> Coding sequence of the single-chain urokinase-plasminogen activator

<400> 4

atg	aga	gcc	ctg	ctg	gcf	cgf	ctg	ctt	ctc	tgc	gtc	ctg	gtc	gtg	agc	48
Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser	
1			5					10				15				
gac	tcc	aaa	ggc	agc	aat	gaa	ctt	cat	caa	gtt	cca	tcg	aac	tgt	gac	96
Asp	Ser	Lys	Gly	Ser	Asn	Glu	Leu	His	Gln	Val	Pro	Ser	Asn	Cys	Asp	
							20			25			30			
tgt	cta	aat	gga	gga	aca	tgt	gtg	tcc	aac	aag	tac	ttc	tcc	aac	att	144
Cys	Leu	Asn	Gly	Gly	Thr	Cys	Val	Ser	Asn	Lys	Tyr	Phe	Ser	Asn	Ile	
						35		40			45					
cac	tgg	tgc	aat	tgc	cca	aag	aaa	ttc	gga	ggg	cag	cac	tgt	gaa	ata	192
His	Trp	Cys	Asn	Cys	Pro	Lys	Lys	Phe	Gly	Gly	Gln	His	Cys	Glu	Ile	
						50		55			60					
gat	aag	tca	aaa	acc	tgc	tat	gag	ggg	aat	ggt	cac	ttt	tac	cga	gga	240
Asp	Lys	Ser	Lys	Thr	Cys	Tyr	Glu	Gly	Asn	Gly	His	Phe	Tyr	Arg	Gly	
						65		70			75		80			
aag	gcc	agc	act	gac	acc	atg	ggc	cgg	ccc	tgc	ccc	tgg	aac	tct	288	
Lys	Ala	Ser	Thr	Asp	Thr	Met	Gly	Arg	Pro	Cys	Leu	Pro	Trp	Asn	Ser	
						85		90			95					
gcc	act	gtc	ctt	cag	caa	acg	tac	cat	gcc	cac	aga	tct	gat	gct	ctt	336
Ala	Thr	Val	Leu	Gln	Gln	Thr	Tyr	His	Ala	His	Arg	Ser	Asp	Ala	Leu	
						100		105			110					
cag	ctg	ggc	ctg	ggg	aaa	cat	aat	tac	tgc	agg	aac	cca	gac	aac	cgg	384
Gln	Leu	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asn	Arg	
						115		120			125					
agg	cga	ccc	tgg	tgc	tat	gtg	cag	gtg	ggc	cta	aag	ccg	ctt	gtc	caa	432
Arg	Arg	Pro	Trp	Cys	Tyr	Val	Gln	Val	Gly	Leu	Lys	Pro	Leu	Val	Gln	
						130		135			140					
gag	tgc	atg	gtg	cat	gac	tgc	gca	gat	gga	aaa	aag	ccc	tcc	tct	cct	480
Glu	Cys	Met	Val	His	Asp	Cys	Ala	Asp	Gly	Lys	Lys	Pro	Ser	Ser	Pro	
						145		150			155		160			
cca	gaa	gaa	tta	aaa	ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	528
Pro	Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	
						165		170			175					
ttt	aag	att	att	ggg	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	576	
Phe	Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	
						180		185			190					
ttt	gcg	gcc	atc	tac	agg	agg	cac	cgg	ggg	ggc	tct	gtc	acc	tac	gtg	624

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val			
195	200	205	
tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac		672	
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His			
210	215	220	
tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt		720	
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly			
225	230	235	240
cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtc		768	
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val			
245	250	255	
gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac		816	
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His			
260	265	270	
cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt		864	
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys			
275	280	285	
gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat		912	
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr			
290	295	300	
aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa		960	
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys			
305	310	315	320
gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt		1008	
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val			
325	330	335	
gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc		1056	
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly			
340	345	350	
tct gaa gtc acc acc aaa atg ctg tgt gct gac cca cag tgg aaa		1104	
Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys			
355	360	365	
aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc		1152	
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu			
370	375	380	
caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt		1200	
Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys			
385	390	395	400
gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta		1248	
Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu			
405	410	415	
ccc tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc		1293	
Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu			
420	425	430	

<210> 5
 <211> 828
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (828)

<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 5

aag ccc tcc tct cct cca gaa gaa tta aaa ttt cag tgt ggc caa aag	48
Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys	
1 5 10 15	
act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc acc atc	96
) Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile	
20 25 30	
gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cac cgg ggg ggc	144
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly	
35 40 45	
tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg	192
Ser Val Thr Tyr Val Cys Gly Ser Leu Ile Ser Pro Cys Trp Val	
50 55 60	
atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac	240
Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr	
65 70 75 80	
atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag	288
Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu	
85 90 95	
) atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct	336
Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala	
100 105 110	
gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc	384
Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser	
115 120 125	
aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc	432
Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys	
130 135 140	
ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc	480
Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile	
145 150 155 160	
act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag	528
Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln	
165 170 175	
ctg aaa atg act gtt gtg aag ctg att tcc cac ccg gag tgt cag cag	576

Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln			
180	185	190	
ccc cac tac tac ggc tct gaa gtc acc acc aaa atg ctg tgt gct gct			624
Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala			
195	200	205	
gac cca cag tgg aaa aca gat tcc tgc cag gga gac tca ggg gga ccc			672
Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro			
210	215	220	
ctc gtc tgt tcc ctc caa ggc cgc atg act ttg act gga att gtg agc			720
Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser			
225	230	235	240
tgg ggc cgt gga tgt gcc ctg aag gac aag cca ggc gtc tac acg aga			768
Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg			
245	250	255	
gtc tca cac ttc tta ccc tgg atc cgc agt cac acc aag gaa gag aat			816
Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn			
260	265	270	
ggc ctg gcc ctc			828
Gly Leu Ala Leu			
275			

<210> 6
<211> 1671
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1) ... (837)
<223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<220>
<221> CDS
<222> (844) ... (1671)
<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 6

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg			48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr			
1	5	10	15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt			96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys			
20	25	30	

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag			144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln			
35	40	45	

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
) aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
) aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
gtg gcg ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
260 265 270	
ctc gtc ctc cgg tgc tcc atg aag ccc tcc tct cct cca gaa	864
Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu	
275 280 285	

gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys 290 295 300	912
att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala 305 310 315 320	960
gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly 325 330 335	1008
ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe 340 345 350	1056
att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser 355 360 365	1104
agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn 370 375 380	1152
ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn 385 390 395 400	1200
gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln 405 410 415	1248
cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp 420 425 430	1296
ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn 435 440 445	1344
tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys 450 455 460	1392
ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Ser Glu 465 470 475 480	1440
gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp 485 490 495	1488
tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly 500 505 510	1536
cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu	1584

515	520	525
-----	-----	-----

aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg	1632	
Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp		
530	535	540

atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc	1671	
Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu		
545	550	555

<210> 7
 <211> 1674
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) ... (837)
) <223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<220>
 <221> CDS
 <222> (847) ... (1674)
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 7
 atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg 48
 Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr
 1 5 10 15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Ser Ser Leu Ala Cys	
20 25 30	

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
---	-----

Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln			
115	120	125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa			432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys			
130	135	140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg			480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu			
145	150	155	160
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg gac aag ctc			528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu			
165	170	175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac			576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His			
180	185	190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc			624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys			
195	200	205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag			672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys			
210	215	220	
ggc gca gtc gct gtc gca gtg gcc cag gtg tgc cgc gtg gta cct ctg			720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu			
225	230	235	240
gtc gca ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc			768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile			
245	250	255	
ctg ctc gac acg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc			816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg			
260	265	270	
ctc gtc ctc cgg tgc tcc atg cag ata tct aag ccc tcc tct cct cca			864
Leu Val Leu Arg Cys Ser Met Gln Ile Ser Lys Pro Ser Ser Pro Pro			
275	280	285	
gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt			912
Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe			
290	295	300	
aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt			960
Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe			
305	310	315	320
gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt			1008
Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys			
325	330	335	
gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc			1056
Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys			
340	345	350	

ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg 355 360 365	1104
tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu 370 375 380	1152
aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac cac Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His 385 390 395 400	1200
aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala 405 410 415	1248
cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn 420 425 430	1296
gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu 435 440 445	1344
aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val 450 455 460	1392
aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser 465 470 475 480	1440
gaa gtc acc acc aaa atg ctg tgt gct gac cca cag tgg aaa aca Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr 485 490 495	1488
gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln 500 505 510	1536
ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala 515 520 525	1584
ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro 530 535 540	1632
tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu 545 550 555	1674

<210> 8
<211> 591
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (591)

<223> Coding sequence of the surfactant protein C precursor

<400> 8

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac	48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	
1 5 10 15	
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
20 25 30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtc ctc atc gtc gtg	144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Leu Ile Val Val	
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc cac atg agc cag aaa cac	192
Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His	
50 55 60	
acg gag atg gtt ctg gag atg agc att ggg gcg ccg gaa gcc cag caa	240
Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln	
65 70 75 80	
cgc ctg gcc ctg agt gag cac ctg gtt acc act gcc acc ttc tcc atc	288
Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile	
85 90 95	
ggc tcc act ggc ctc gtg gtg tat gac tac cag cag ctg ctg atc gcc	336
Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala	
100 105 110	
tac aag cca gcc cct ggc acc tgc tgc tac atc atg aag ata gct cca	384
Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro	
115 120 125	
gag agc atc ccc agt ctt gag gct ctc act aga aaa gtc cac aac ttc	432
Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe	
130 135 140	
cag atg gaa tgc tct ctg cag gcc aag ccc gca gtg cct acg tct aag	480
Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys	
145 150 155 160	
ctg ggc cag gca gag ggg cga gat gca ggc tca gca ccc tcc gga ggg	528
Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly	
165 170 175	
gac ccg gcc ttc ctg ggc atg gcc gtg agc acc ctg tgt ggc gag gtg	576
Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val	
180 185 190	
ccg ctc tac tac atc	591
Pro Leu Tyr Tyr Ile	
195	

<210> 9
 <211> 174
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (174)
 <223> Coding sequence of the surfactant protein C precursor lacking the C-terminal propeptide

<400> 9

atg	gat	gtg	ggc	agc	aaa	gag	gtc	ctg	atg	gag	agc	ccg	ccg	gac	tac	48
Met	Asp	Val	Gly	Ser	Lys	Glu	Val	Leu	Met	Glu	Ser	Pro	Pro	Asp	Tyr	
1		5						10						15		

tcc	gca	gct	ccc	cgg	ggc	cga	ttt	ggc	att	ccc	tgc	tgc	cca	gtg	cac	96
Ser	Ala	Ala	Pro	Arg	Gly	Arg	Phe	Gly	Ile	Pro	Cys	Cys	Pro	Val	His	
		20						25						30		

ctg	aaa	cgc	ctt	ctt	atc	gtg	gtg	gtg	gtg	gtc	ctc	atc	gtc	gtg	144	
Leu	Lys	Arg	Leu	Leu	Ile	Val	Leu	Ile	Val	Val						
		35				40							45			

gtg	att	gtg	gga	gcc	ctg	ctc	atg	ggt	ctc						174
Val	Ile	Val	Gly	Ala	Leu	Leu	Met	Gly	Leu						
		50				55									

<210> 10
 <211> 105
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (105)
 <223> Coding sequence of the mature surfactant protein C

<400> 10

ttt	ggc	att	ccc	tgc	tgc	cca	gtg	cac	ctg	aaa	cgc	ctt	ctt	atc	gtg	48
Phe	Gly	Ile	Pro	Cys	Cys	Pro	Val	His	Leu	Lys	Arg	Leu	Leu	Ile	Val	
1		5						10						15		

gtg	gtg	gtg	gtg	gtc	ctc	atc	gtc	gtg	gtg	att	gtg	gga	gcc	ctg	ctc	96
Val	Val	Val	Val	Leu	Ile	Val	Val	Val	Ile	Val	Gly	Ala	Leu	Leu		
		20				25							30			

atg	ggt	ctc													105
Met	Gly	Leu													
		35													

<210> 11
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1686)

<223> Coding sequence of the tissue-plasminogen activator

<400> 11

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly	
1 5 10 15	
gca gtc ttc gtt tcg ccc agc cag gaa atc cat gcc cga ttc aga aga	96
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg	
20 25 30	
gga gcc aga tct tac caa gtg atc tgc aga gat gaa aaa acg cag atg	144
Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met	
35 40 45	
ata tac cag caa cat cag tca tgg ctg cgc cct gtg ctc aga agc aac	192
Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn	
50 55 60	
cgg gtg gaa tat tgc tgg tgc aac agt ggc agg gca cag tgc cac tca	240
Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser	
65 70 75 80	
gtg cct gtc aaa agt tgc agc gag cca agg tgt ttc aac ggg ggc acc	288
Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr	
85 90 95	
tgc cag cag gcc ctg tac ttc tca gat ttc gtg tgc cag tgc ccc gaa	336
Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu	
100 105 110	
gga ttt gct ggg aag tgc tgt gaa ata gat acc agg gcc acg tgc tac	384
Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr	
115 120 125	
gag gac cag ggc atc agc tac agg ggc acg tgg agc aca gcg gag agt	432
Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser	
130 135 140	
ggc gcc gag tgc acc aac tgg aac agc agc gcg ttg gcc cag aag ccc	480
Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro	
145 150 160 165	
tac agc ggg cgg agg cca gat gcc atc agg ctg ggc ctg ggg aac cac	528
Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His	
170 175 180	
aac tac tgc aga aac cca gat cga gac tca aag ccc tgg tgc tac gtc	576
Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val	
185 190 195	
ttt aag gcg ggg aag tac agc tca gag ttc tgc agc acc cct gcc tgc	624
Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys	
200 205 205	

tct gag gga aac agt gac tgc tac ttt ggg aat ggg tca gcc tac cgt Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg 210 215 220	672
ggc acg cac agc ctc acc gag tcg ggt gcc tcc tgc ctc ccg tgg aat Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn 225 230 235 240	720
tcc atg atc ctg ata ggc aag gtt tac aca gca cag aac ccc agt gcc Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala 245 250 255	768
cag gca ctg ggc ctg ggc aaa cat aat tac tgc cgg aat cct gat ggg Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly 260 265 270	816
gat gcc aag ccc tgg tgc cac gtg ctg aag aac cgc agg ctg acg tgg Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp 275 280 285	864
) gag tac tgt gat gtg ccc tcc tgc tcc acc tgc ggc ctg aga cag tac Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr 290 295 300	912
agc cag cct cag ttt cgc atc aaa gga ggg ctc ttc gcc gac atc gcc Ser Gln Pro Gln Phe Arg Ile Lys Gly Leu Phe Ala Asp Ile Ala 305 310 315 320	960
tcc cac ccc tgg cag gct gcc atc ttt gcc aag cac agg agg tcg ccc Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro 325 330 335	1008
) gga gag cgg ttc ctg tgc ggg ggc ata ctc atc agc tcc tgc tgg att Gly Glu Arg Phe Leu Cys Gly Ile Leu Ile Ser Ser Cys Trp Ile 340 345 350	1056
ctc tct gcc gcc cac tgc ttc cag gag agg ttt ccg ccc cac cac ctg Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu 355 360 365	1104
) acg gtg atc ttg ggc aga aca tac cgg gtg gtc cct ggc gag gag gag Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu 370 375 380	1152
cag aaa ttt gaa gtc gaa aaa tac att gtc cat aag gaa ttc gat gat Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp 385 390 395 400	1200
gac act tac gac aat gac att gcg ctg ctg cag ctg aaa tcg gat tcg Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser 405 410 415	1248
tcc cgc tgt gcc cag gag agc agc gtg gtc cgc act gtg tgc ctt ccc Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro 420 425 430	1296
ccg gcg gac ctg cag ctg ccg gac tgg acg gag tgt gag ctc tcc ggc Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly	1344

435	440	445	
tac ggc aag cat gag gcc ttg tct cct ttc tat tcg gag cgg ctg aag Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys			1392
450	455	460	
gag gct cat gtc aga ctg tac cca tcc agc cgc tgc aca tca caa cat Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His			1440
465	470	475	480
tta ctt aac aga aca gtc acc gac aac atg ctg tgt gct gga gac act Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr			1488
485	490	495	
cgg agc ggc ggg ccc cag gca aac ttg cac gac gcc tgc cag ggc gat Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp			1536
500	505	510	
tcg gga ggc ccc ctg gtg tgt ctg aac gat ggc cgc atg act ttg gtg Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val			1584
515	520	525	
ggc atc atc agc tgg ggc ctg ggc tgt gga cag aag gat gtc ccg ggt Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly			1632
530	535	540	
gtg tac acc aag gtt acc aac tac cta gac tgg att cgt gac aac atg Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met			1680
545	550	555	560
cga ccg Arg Pro			1686

<210> 12
<211> 1158
<212> DNA
<213> Artificial Sequence

<220>
<221> sig_peptide
<222> (1) ... (69)
<223> Signal sequence of the surfactant protein B

<220>
<221> CDS
<222> (76) ... (312)
<223> Coding sequence of the mature surfactant protein B

<220>
<221> CDS
<222> (313) ... (1140)
<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>
<221> CDS
<222> (1141) ... (1158)
<223> Hexahistidin affinity tag

<400> 12

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr	48
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg ttc ccc att cct ctc ccc tat Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr	96
20 25 30	
tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro	144
35 40 45	
aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro	192
50 55 60	
) ctg gtg gcg ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val	240
65 70 75 80	
atc ctg ctc gac acg ctg ggc cgc atg ctg ccc cag ctg gtc tgc Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys	288
85 90 95	
cgc ctc gtc ctc cgg tgc tcc atg aag ccc tcc tct cct cca gaa gaa Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu	336
100 105 110	
tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile	384
115 120 125	
) att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc Ile Gly Gly Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala	432
130 135 140	
atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly	480
145 150 155 160	
agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile	528
165 170 175	
gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg	576
180 185 190	
) ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu	624
195 200 205	
atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac gac Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp	672
210 215 220	

att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro 225 230 235 240	720
tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat ccc Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro 245 250 255	768
cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser 260 265 270	816
acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu 275 280 285	864
att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa gtc Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val 290 295 300	912
acc acc aaa atg ctg tgt gct gac cca cag tgg aaa aca gat tcc Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser 305 310 315 320	960
tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg 325 330 335	1008
atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys 340 345 350	1056
gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile 355 360 365	1104
cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc cat cat cat cat Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His 370 375 380	1152
cat cat His His 385	1158

<210> 13
<211> 1149
<212> DNA
<213> Artificial Sequence

<220>
<221> sig_peptide
<222> (1) ... (60)
<223> Signal sequence of the urokinase plasminogen activator

<220>
<221> CDS
<222> (67) ... (894)

<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>

<221> CDS

<222> (895) ... (1131)

<223> Coding sequence of the mature surfactant protein B

<220>

<221> CDS

<222> (1132) ... (1149)

<223> Hexahistidin affinity tag

<400> 13

atg	aga	gcc	ctg	ctg	gcg	cgc	ctg	ctt	ctc	tgc	gtc	ctg	gtc	gtg	agc	48
Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser	
1		5						10						15		
gac	tcc	aaa	ggc	agc	aat	aag	ccc	tcc	tct	cct	cca	gaa	gaa	tta	aaa	96
Asp	Ser	Lys	Gly	Ser	Asn	Lys	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Glu	Leu	Lys
20							25						30			
ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	ttt	aag	att	att	ggg	144
Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly	
35							40						45			
gga	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	ttt	gcg	gcc	atc	tac	192
Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	Ile	Tyr	
50							55						60			
agg	agg	cac	cgg	ggg	ggc	tct	gtc	acc	tac	gtg	tgt	gga	ggc	agc	ctc	240
Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu	
65							70						80			
atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	tgc	ttc	att	gat	tac	288
Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr	
85							90						95			
cca	aag	aag	gag	gac	tac	atc	gtc	tac	ctg	ggt	cgc	tca	agg	ctt	aac	336
Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn	
100							105						110			
tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	gaa	aac	ctc	atc	cta	384
Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu	
115							120						125			
cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	cac	aac	gac	att	gcc	432
His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala	
130							135						140			
ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	gcg	cag	cca	tcc	cgg	480
Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg	
145							150						155			160
act	ata	cag	acc	atc	tgc	ctg	ccc	tcg	atg	tat	aac	gat	ccc	cag	ttt	528
Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe	
165								170						175		

ggc aca aac tgt gag atc act ggc ttt gga aaa gag aat tct acc gac	576
Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp	
180 185 190	
tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg att tcc	624
Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile Ser	
195 200 205	
cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa gtc acc acc	672
His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr	
210 215 220	
aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat tcc tgc cag	720
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln	
225 230 235 240	
gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc atg act	768
Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr	
245 250 255	
ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag gac aag	816
Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys	
260 265 270	
cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc cgc agt	864
Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser	
275 280 285	
cac acc aag gaa gag aat ggc ctg gcc ctc ttc ccc att cct ctc ccc	912
His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro	
290 295 300	
tat tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att	960
Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile	
305 310 315 320	
ccc aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta	1008
Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val	
325 330 335	
cct ctg gtg gcg ggc atc tgc cag tgc ctg gct gag cgc tac tcc	1056
Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser	
340 345 350	
gtc atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc	1104
Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val	
355 360 365	
tgc cgc ctc gtc ctc cgg tgc tcc atg cat cat cat cat cat cat	1149
Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His	
370 375 380	